

FIG. 1A

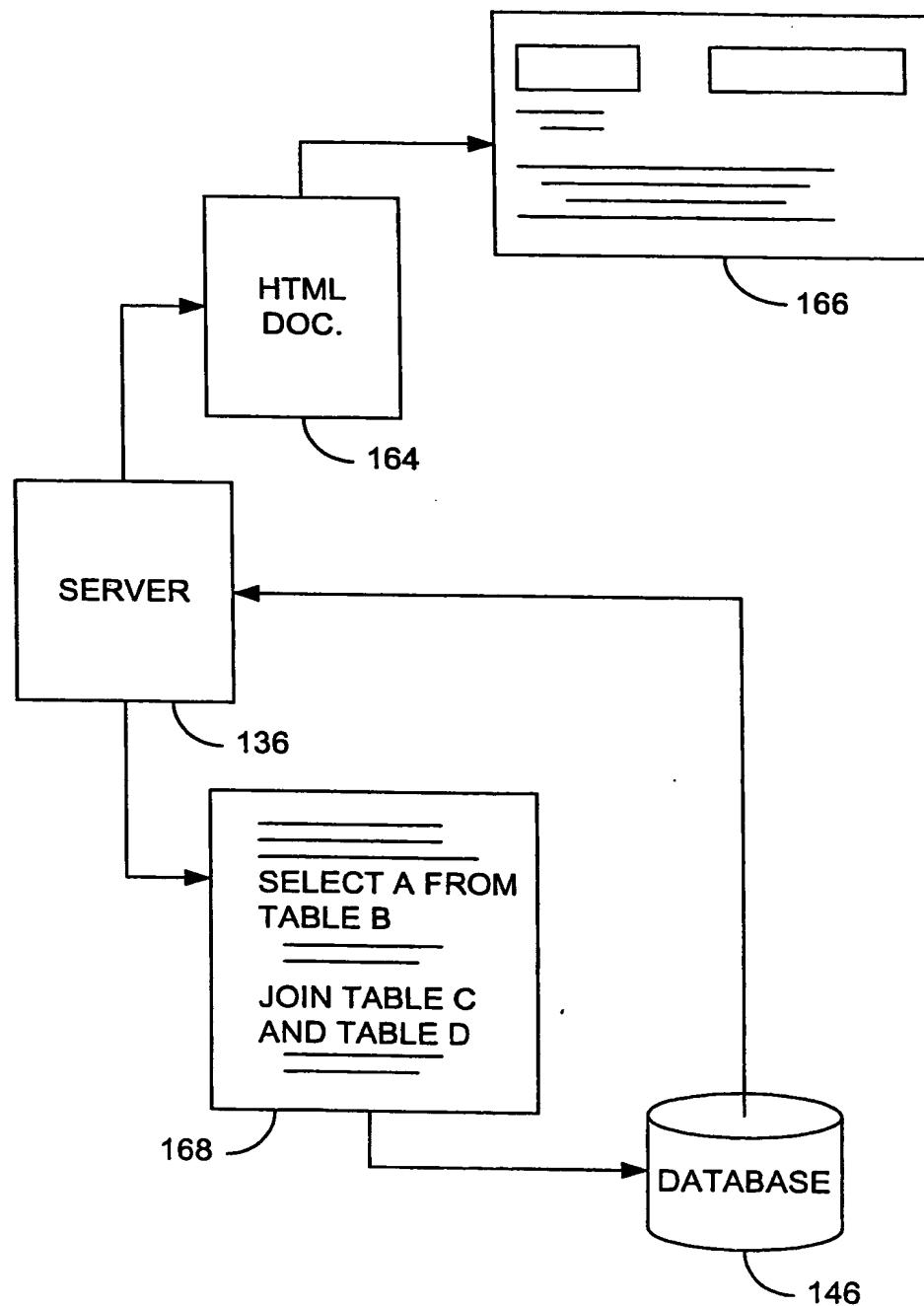


FIG. 1B

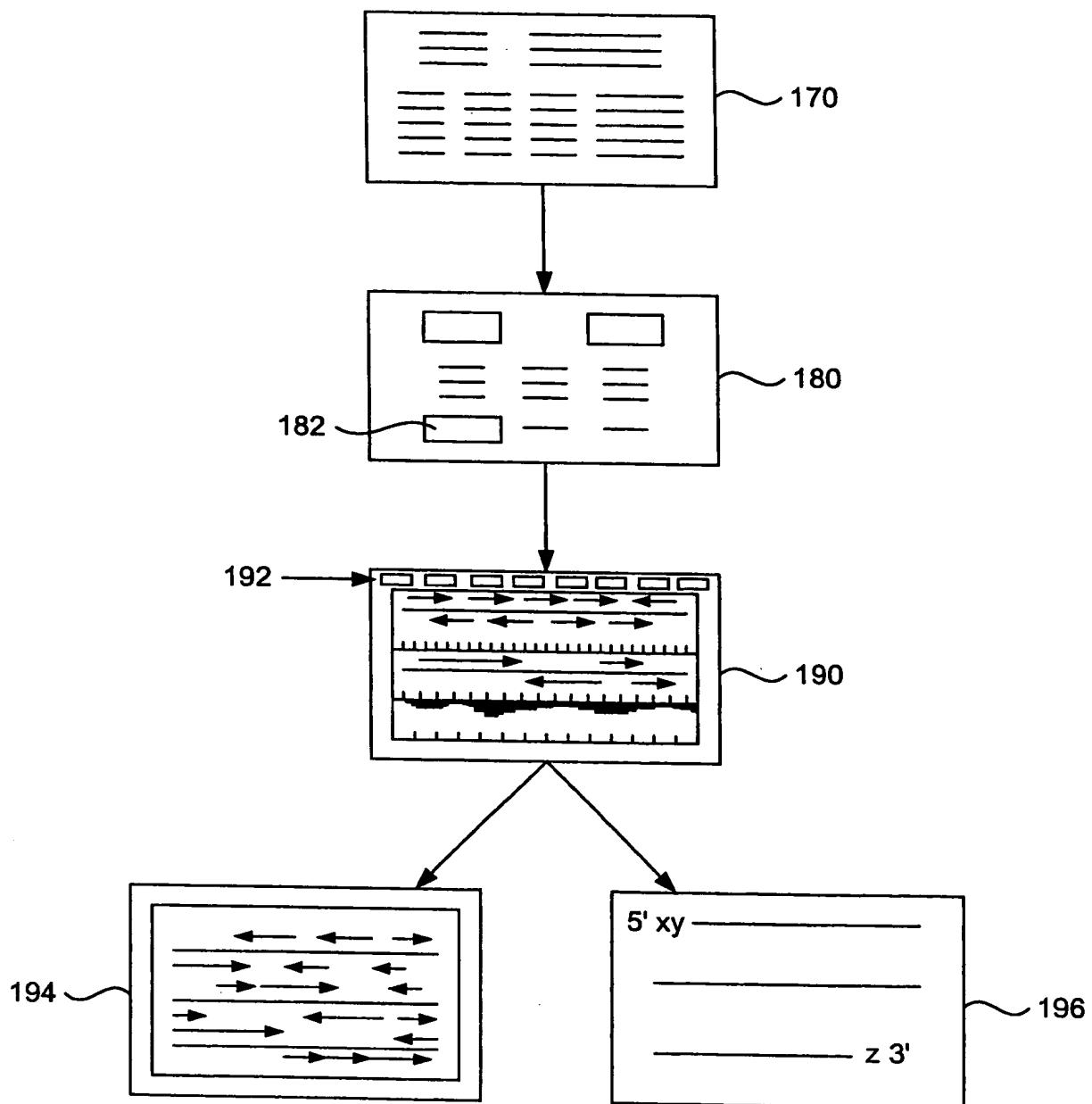


FIG. 1C

Contig Results						
Library :	SAUREU01	Staphylococcus aureus	Contigs: 48	Contigs ORFs: 134	Base Pairs Selected: 1 to 138277	Seqs...
Contig:	SAU1c0039	Length: 138277 bp	Segs: 1846	Hit Organism	E-Value	Base Pairs
LocusID	Hit ID	Hit Description				
SAU102730	g26333184	Yfth0	Bacillus subtilis	3.4e-51	22-2169 (-)	8
SAU103442		LUR	Bacillus subtilis	4.8e-62	2170-2722 (-)	0
SAU100689	g26333977	similar to hypothetical proteins	Bacillus subtilis	3.2e-39	2723-3559 (+)	24
SAU102070	g26333978	ribonuclease H	Bacillus subtilis	6.8e-123	3594-4352 (+)	34
SAU100241	g2462967	putative succinyl-CoA synthetase beta ch	Bacillus subtilis	2.9e-97	4467-5621 (+)	35
SAU100242	g26333982	succinyl-CoA synthetase (alpha subunit)	Bacillus subtilis	4.8e-23	5655-6542 (+)	35
SAU102767	g3767593	Lyn	Staphylococcus	6849-6998 (+)	3	7
SAU101151	g3767595	Eph	Staphylococcus	7029-8270 (+)	13	18
SAU101152	g26333984	ORF4	Staphylococcus	3.5e-109	8514-9314 (+)	36
SAU101153	g2462971	DNA Topoisomerase I	Bacillus subtilis	0	9497-11563 (+)	48
SAU101154	g26333986	Gid protein	Bacillus subtilis	0	11728-13026 (+)	43
SAU101155	g26333987	Integrase/recombinase	Bacillus subtilis	7.1e-51	13440-14333 (+)	38
SAU101156	g26333987	beta-type subunit of the 20S proteasome	Bacillus subtilis	9.7e-52	14348-14881 (+)	21
SAU101157	g26333988	ATP-dependent Clp protease-like	Bacillus subtilis	7.4e-95	14971-16350 (+)	40
SAU101158	g26333989	transcriptional regulator	Bacillus subtilis	1.3e-62	16378-17139 (+)	9
SAU100275	g26334021	ribosomal protein S2	Bacillus subtilis	2.8e-73	17493-18200 (+)	47

FIG. 2
200

Locus Query - Netscape

Locus Information

Main Menu Organelle Genome Contig Summary Contig Locus Info Proteins Comparisons Southern Sequences Help

Search by LocusID: Display: Locus Details 5 Loci around the selected Locus

Graphical Viewer ~ 302

Locus ID: SAU100241 **Type:** Homology
C ntig ID: SAU1c0039 **Position:** 5 of 150
Amino Acids: 385 **Nucleotides:** 1155 **Seqs:** 13
Homologs: 46 **Libs:** 35

Top hits: FASTA of ORF against pagenpept110

Hit ID	Hit Description	Hit Organism	E-Value	ORF Coverage
g2462967	putative succinyl-CoA synthetase beta ch	Bacillus subtili	6.8e-123	100%
g2633981	succinyl-CoA synthetase (beta subunit)	Bacillus subtili	6.8e-123	100%

300

FIG. 3

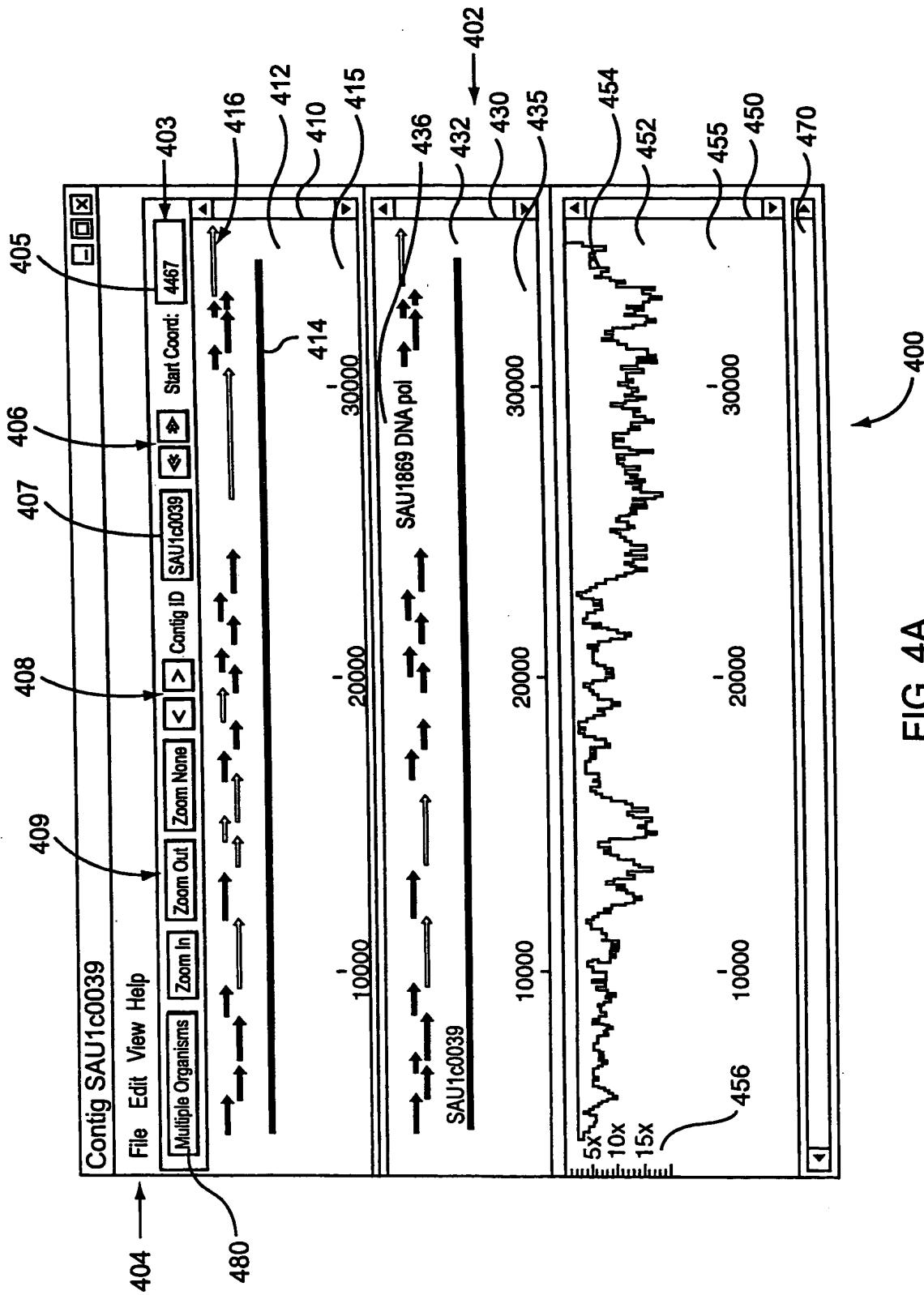


FIG. 4A

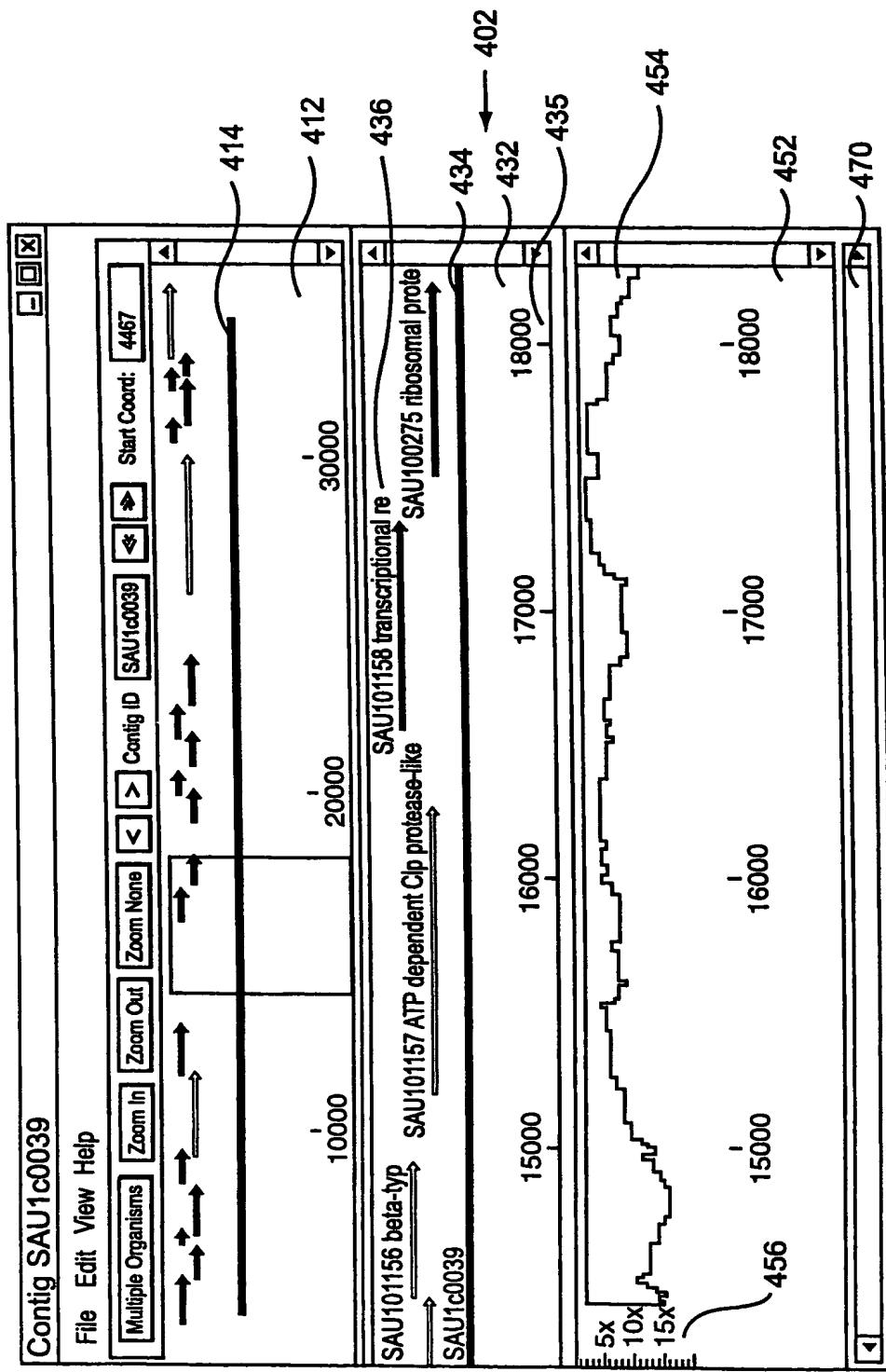


FIG. 4B

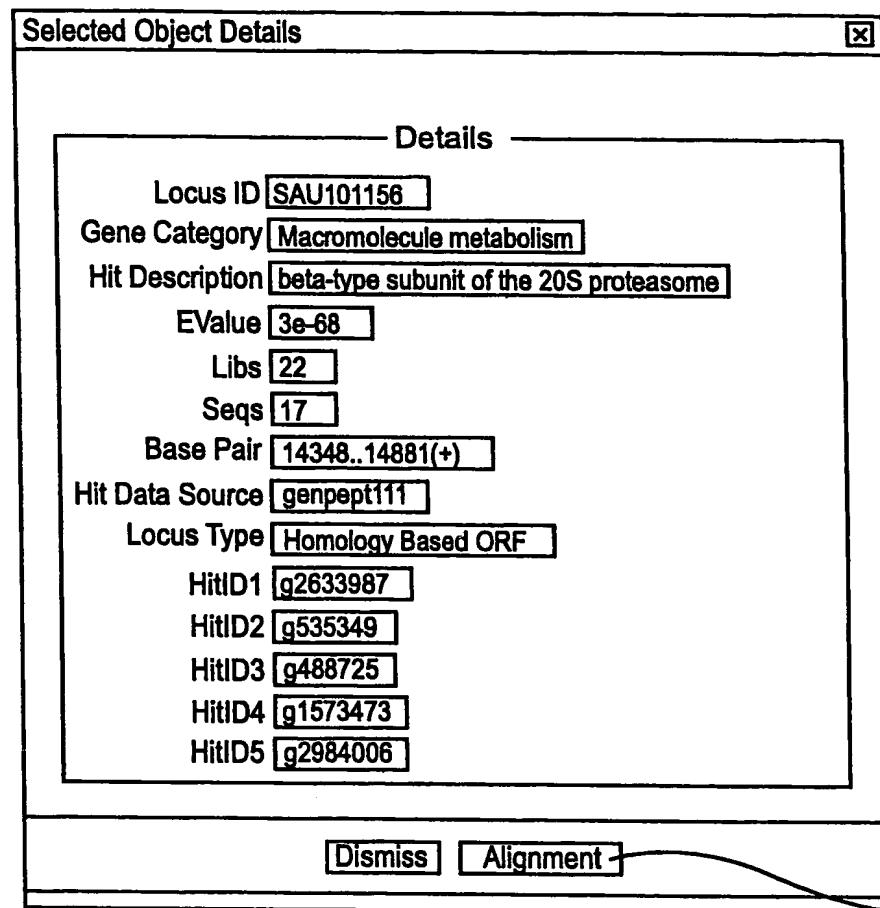


FIG. 5A

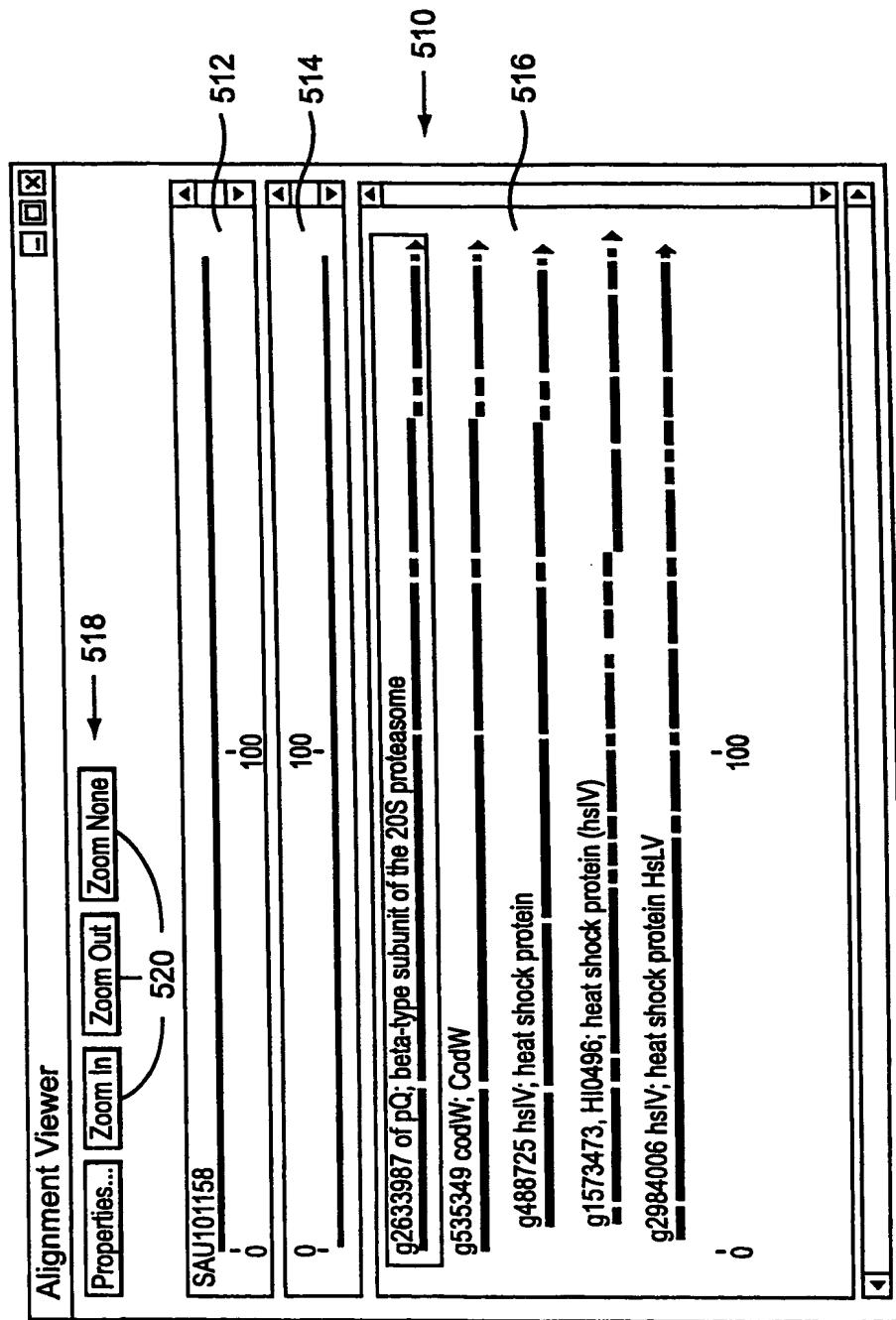


FIG. 5B

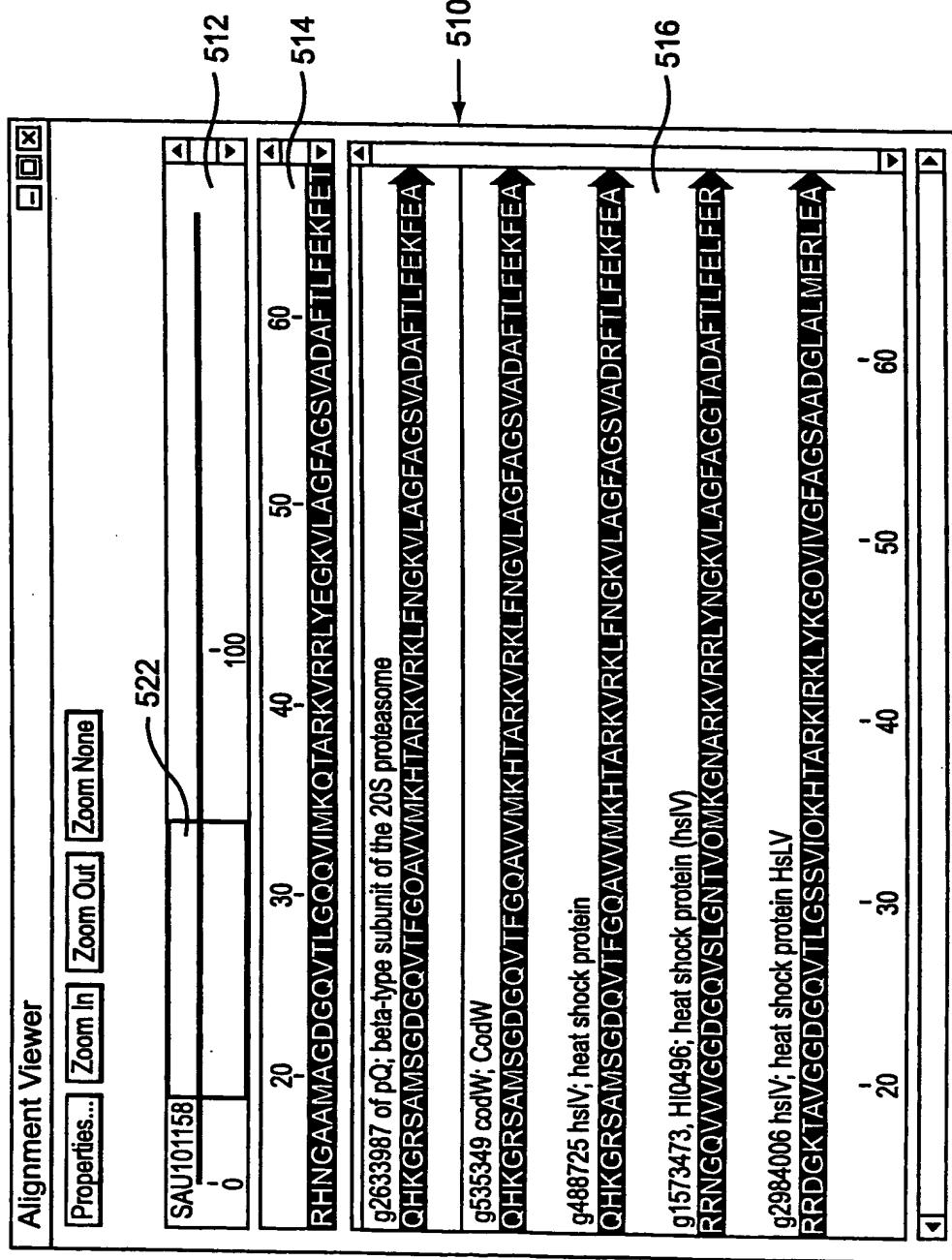


FIG. 5C

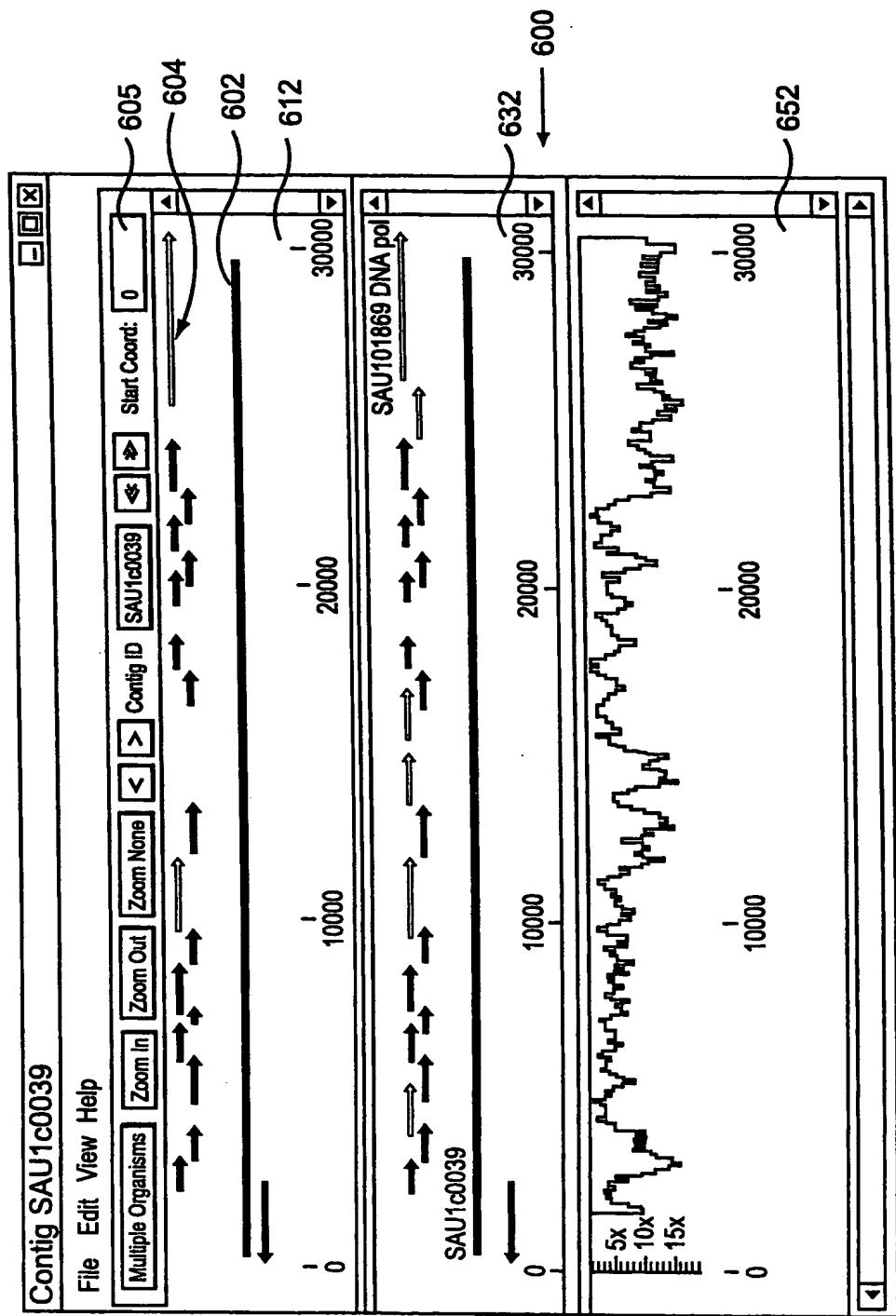


FIG. 6

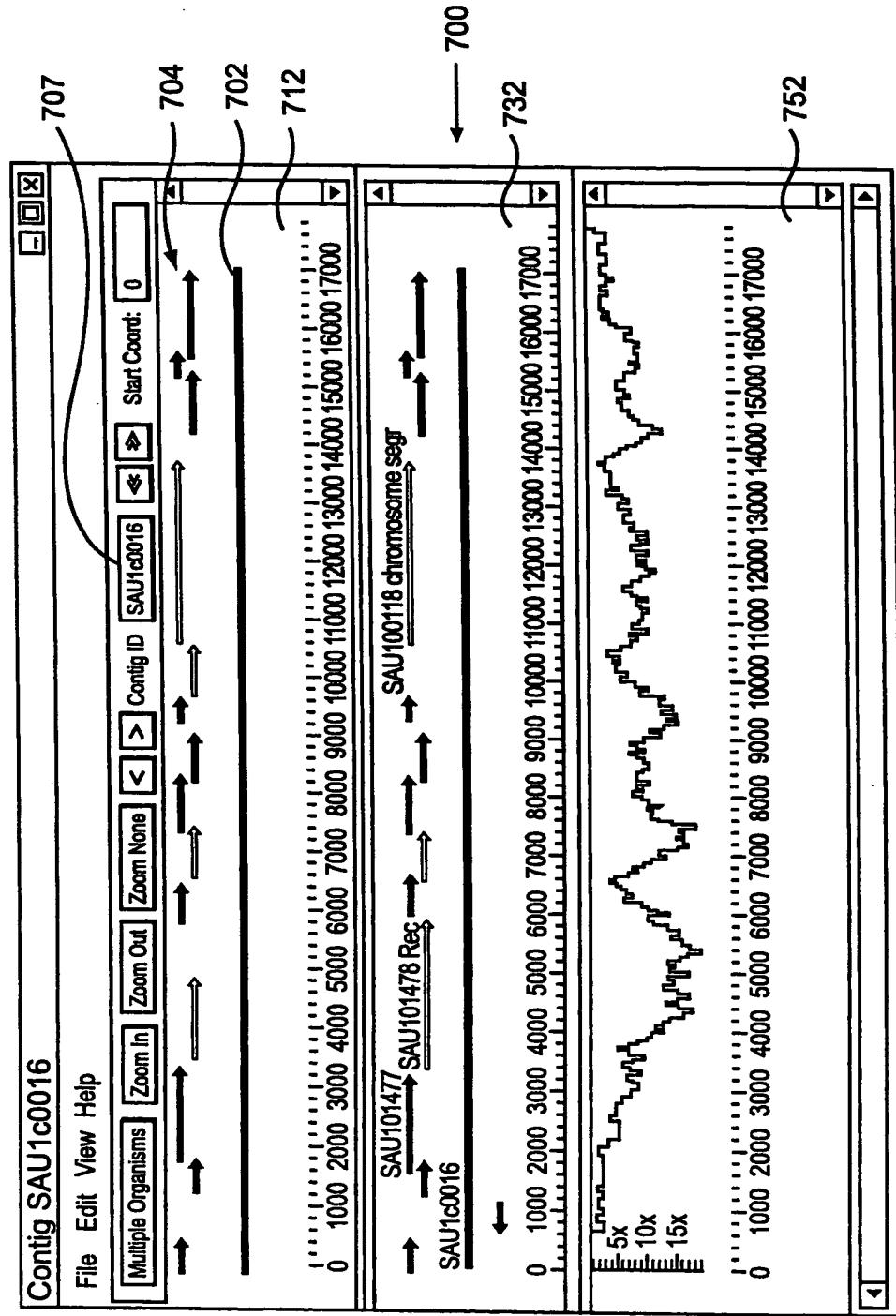


FIG. 7

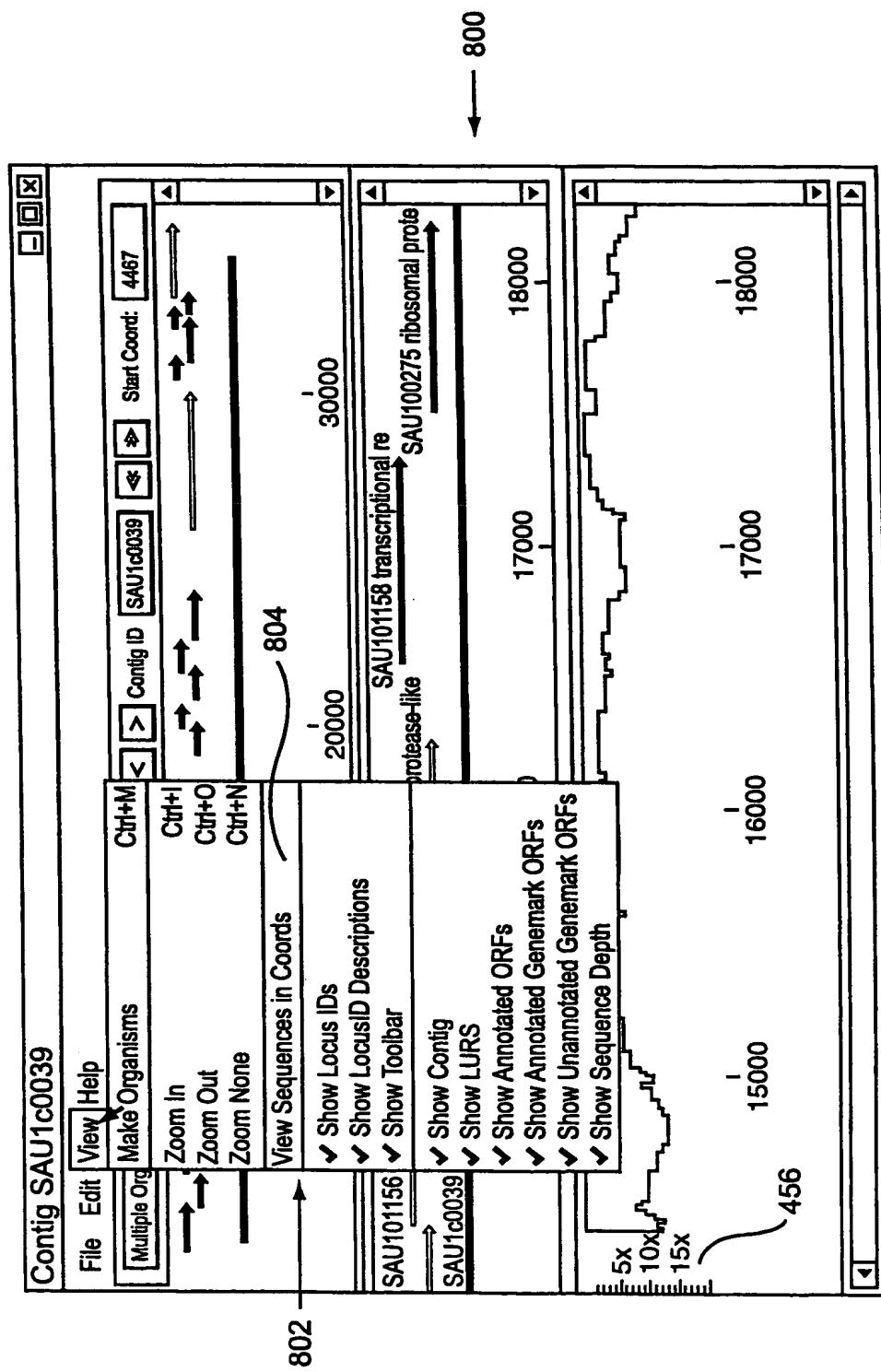


FIG. 8A

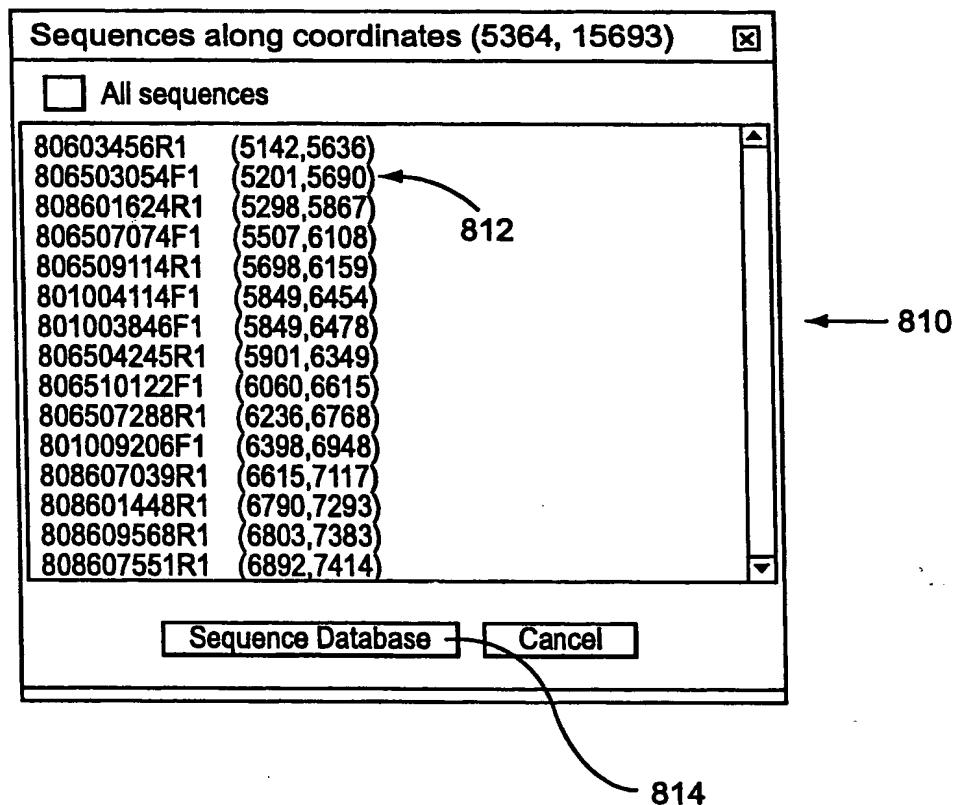


FIG. 8B

Sequence Retrieval Results - Netscape

Sequence Retrieval Results

Main Menu Org Info Genome Contig Summary Contig Locus Info Proteins Comparisons Southern Sequences Life Tools
 Help

Retrieval BLAST BLAST2 FASTA ClustalW GCG Assembly Phrap Translation Sequence Info

>806503054F1 saureu01

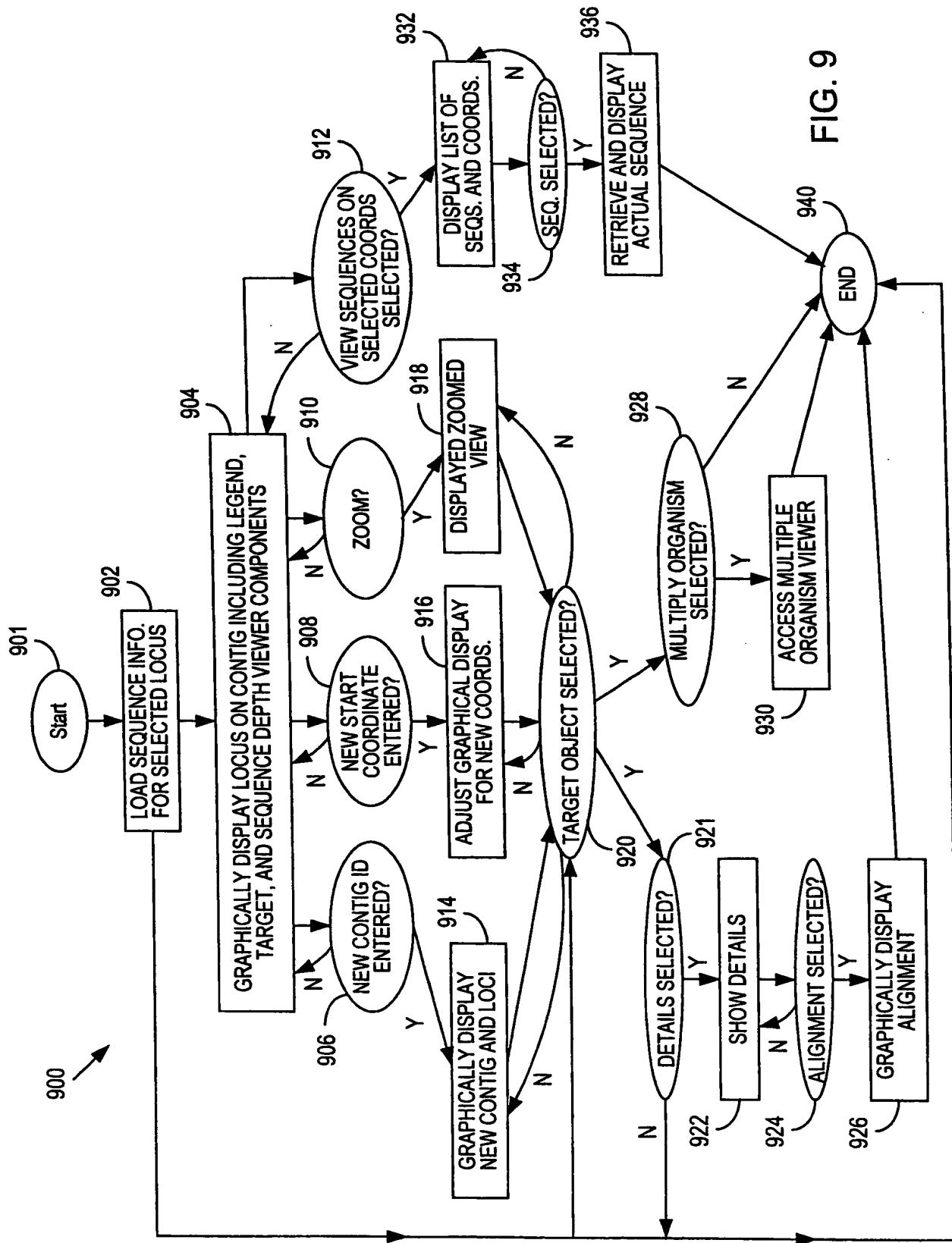
GTCTAACATGATTATCATACATTGCATTAGATGGGTGACATCGGATGTATGGTGAATGGTGCAGGTTAGCCAT
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 AGAAAAAAAGTAACTGAAGCATTAAATCATTTAGGTGATGAAAATGTTAAAGGTATTGTAACATTTCGG
 TGGCATTATGAAATGTTGATGTTATCGCAGAAGGTAAAGGAGTAGATTAACTTACACT
 AGTTGTACGGCTTAGAAGGTACAAATGTTGAGTTAGGTAAAAGACTCTAAAGACTCAGGATTGCAATTGAAAC
 AGCAGCAACATGGCTGAAGGTGCACAAAAATTGTTAAACTAGTCAAAAGGATAAGGAAAGGATGGGAGCAC
 TAAGATGAGTGTTTATAGATAAGAATACTAAAGTAAT

822

820

Submit sequences to: BLAST Submit Reset

FIG. 8C



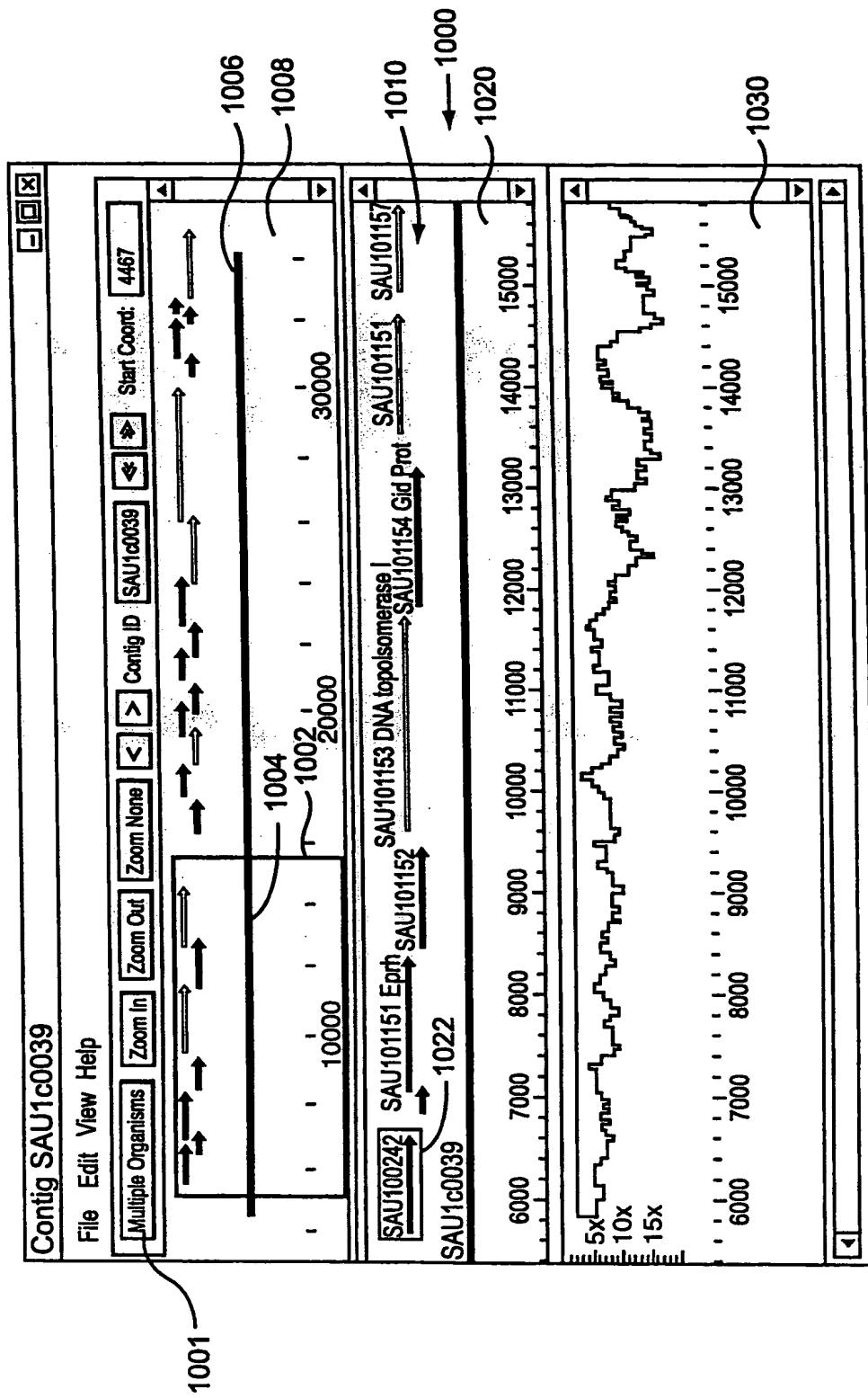


FIG. 10A

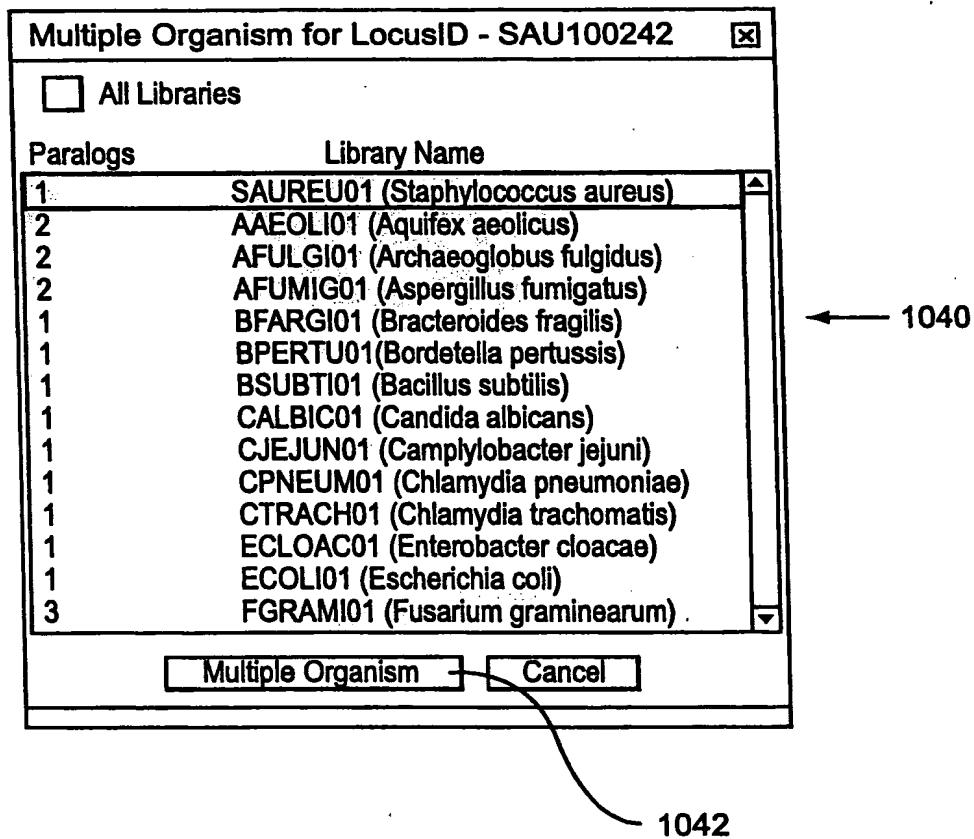


FIG. 10B

Multiple Organism for LocusID - SAU100242

Display all Loci

LocusID	Hit Description
SAU100242	succinyl-CoA synthetase (alpha subunit)
CAL07951	probable succinyl-coa ligase
PRT102068	succinyl-CoA synthetase, alpha subunit
SAU200294	succinyl-CoA synthetase (alpha subunit)
SEP100435	succinyl-CoA synthetase (alpha subunit)
SEP100614	ORF1
SHA100180	succinyl-CoA synthetase (alpha subunit)

← 1045

Multiple Organism 1046

FIG. 10C

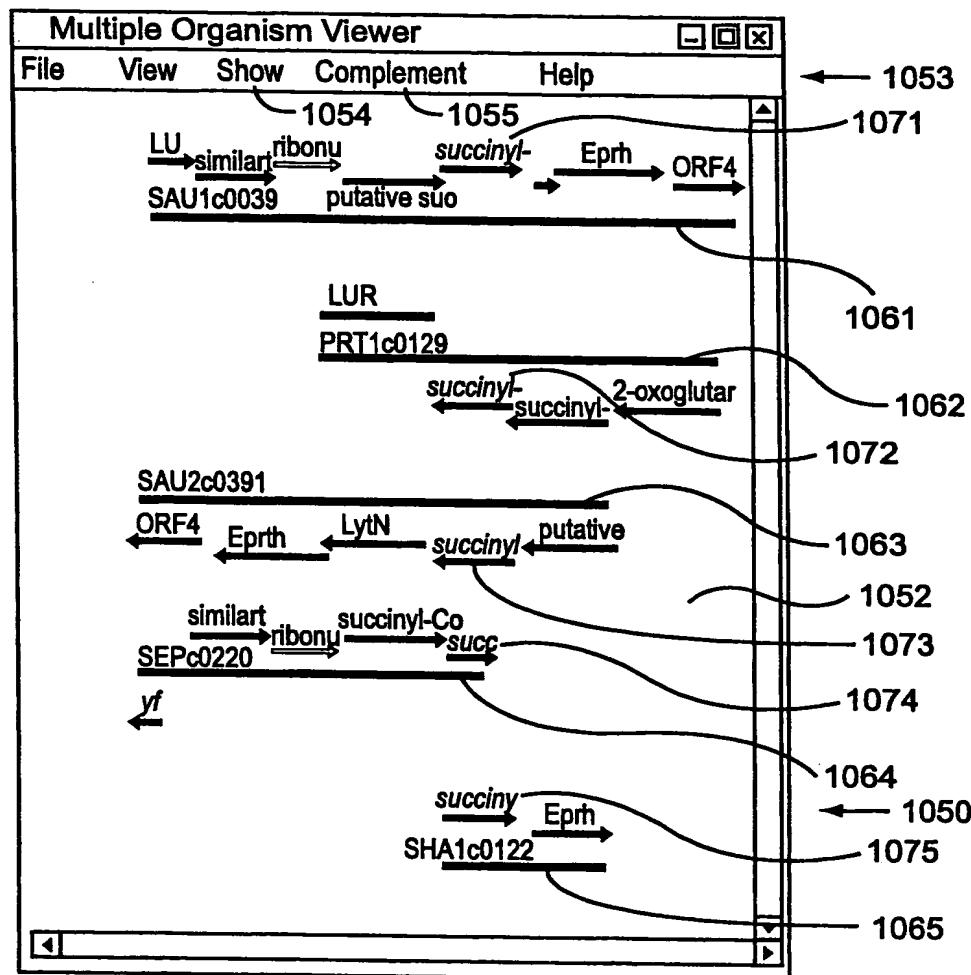


FIG. 10D

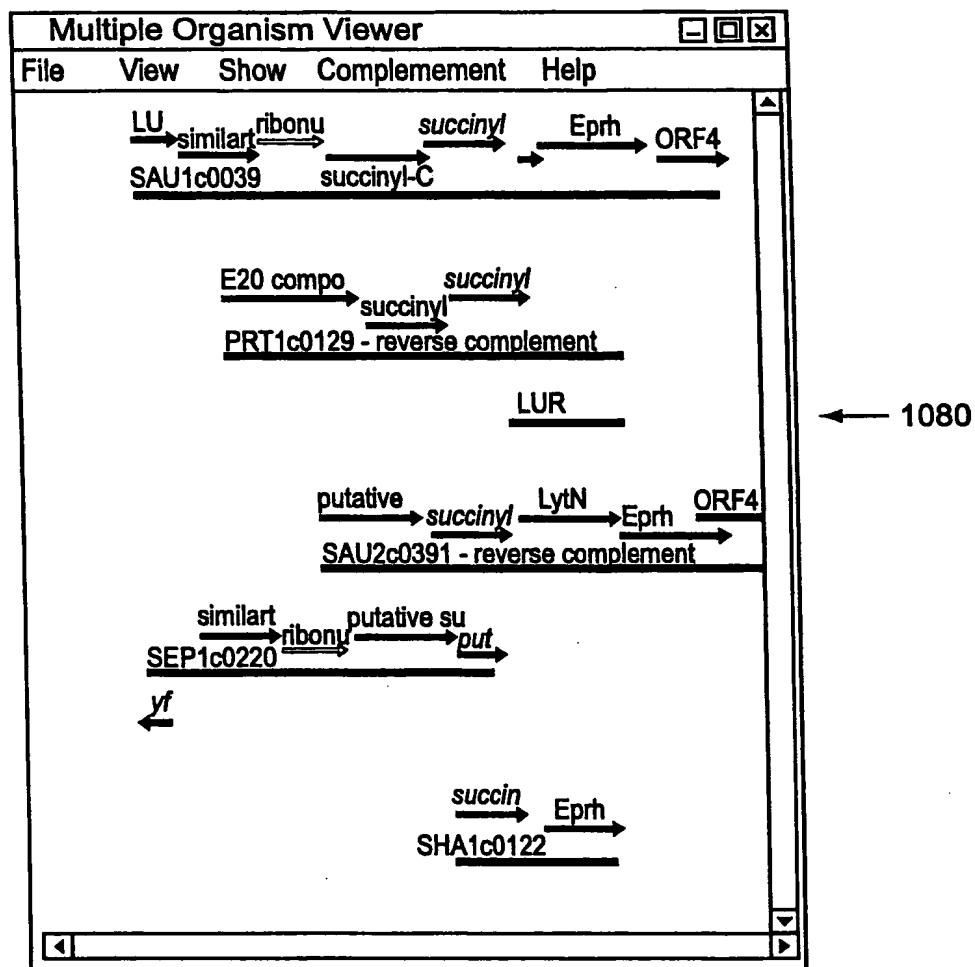


FIG. 10E

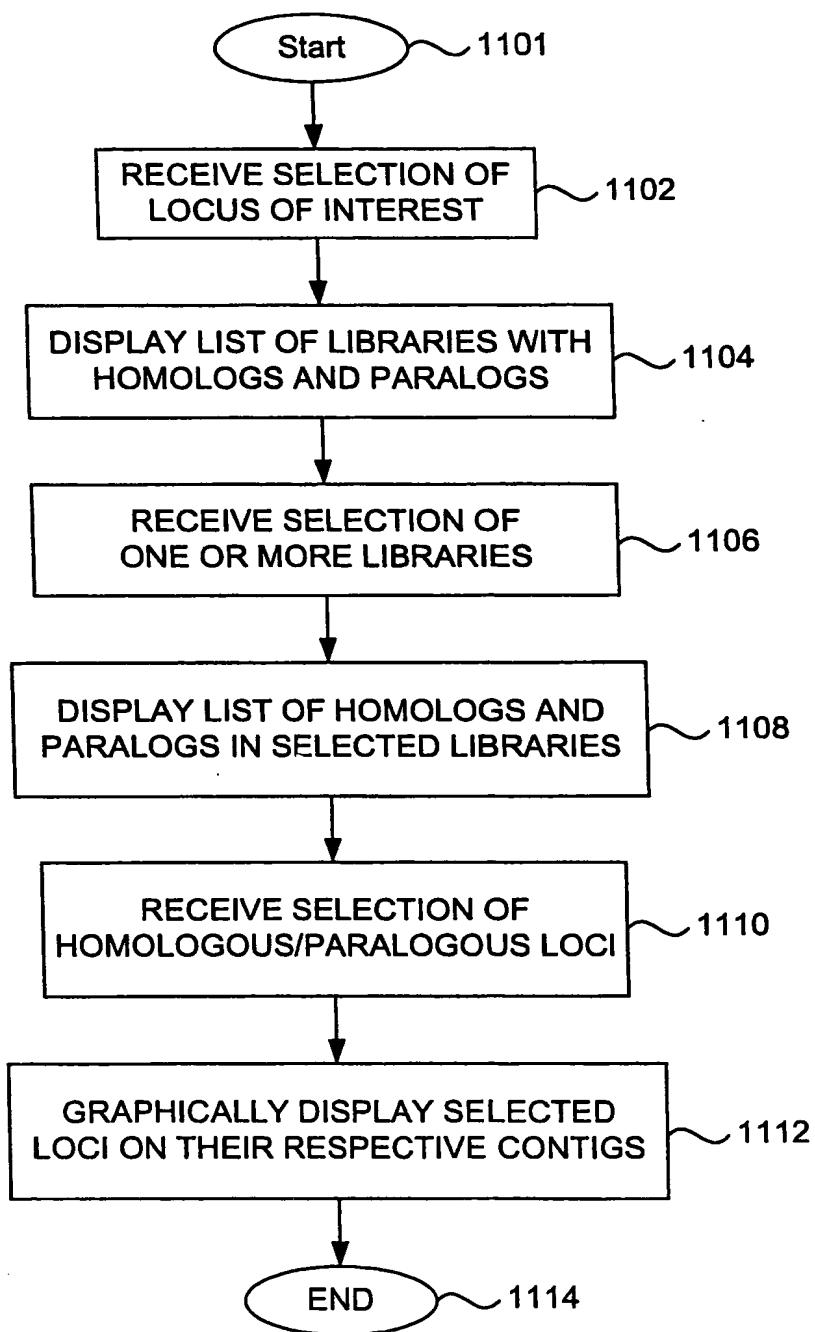


FIG. 11